<110>   Protein Design Labs, Inc.
        Afar, et al.

<120>   Methods of Prognosis of Prostate Cancer

<130>   05882.0132.NPUS01

<140>   10/603,505
<141>   2003-06-24

<160>   2

<170>   PatentIn version 3.2

<210>   1
<211>   1104
<212>   PRT
<213>   Homo sapiens

<400>   1

Met Ser Phe Arg Ala Ala Arg Leu Ser Met Arg Asn Arg Arg Asn Asp
1   5   10   15

Thr Leu Asp Ser Thr Arg Thr Leu Tyr Ser Ser Ala Ser Arg Ser Thr
            20   25   30

Asp Leu Ser Tyr Ser Glu Ser Asp Leu Val Asn Phe Ile Gln Ala Asn
        35   40   45

Phe Lys Lys Arg Glu Cys Val Phe Phe Thr Lys Asp Ser Lys Ala Thr
    50   55   60

Glu Asn Val Cys Lys Cys Gly Tyr Ala Gln Ser Gln His Met Glu Gly
65   70   75   80

Thr Gln Ile Asn Gln Ser Glu Lys Trp Asn Tyr Lys Lys His Thr Lys
                85   90   95

Glu Phe Pro Thr Asp Ala Phe Gly Asp Ile Gln Phe Glu Thr Leu Gly
            100   105   110

Lys Lys Gly Lys Tyr Ile Arg Leu Ser Cys Asp Thr Asp Ala Glu Ile
        115   120   125

Leu Tyr Glu Leu Leu Thr Gln His Trp His Leu Lys Thr Pro Asn Leu
    130   135   140

Val Ile Ser Val Thr Gly Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg

Met Arg Lys Ile Phe Ser Arg Leu Ile Tyr Ile Ala Gln Ser Lys Gly
                 165   170   175

Ala Trp Ile Leu Thr Gly Gly Thr His Tyr Gly Leu Met Lys Tyr Ile
                 180   185   190

Gly Glu Val Val Arg Asp Asn Thr Ile Ser Arg Ser Ser Glu Glu Asn
             195   200   205

Ile Val Ala Ile Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp
         210   215   220

Thr Leu Ile Arg Asn Cys Asp Ala Glu Gly Tyr Phe Leu Ala Gln Tyr
225   230   235   240

Leu Met Asp Asp Phe Thr Arg Asp Pro Leu Tyr Ile Leu Asp Asn Asn
                 245   250   255

His Thr His Leu Leu Leu Val Asp Asn Gly Cys His Gly His Pro Thr
             260   265   270

Val Glu Ala Lys Leu Arg Asn Gln Leu Glu Lys Tyr Ile Ser Glu Arg
         275   280   285

Thr Ile Gln Asp Ser Asn Tyr Gly Gly Lys Ile Pro Ile Val Cys Phe
     290   295   300

Ala Gln Gly Gly Gly Lys Glu Thr Leu Lys Ala Ile Asn Thr Ser Ile
305   310   315   320

Lys Asn Lys Ile Pro Cys Val Val Val Glu Gly Ser Gly Gln Ile Ala
                 325   330   335

Asp Val Ile Ala Ser Leu Val Glu Val Glu Asp Ala Leu Thr Ser Ser
             340   345   350

Ala Val Lys Glu Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg
         355   360   365

Leu Pro Glu Glu Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile
     370   375   380

Leu Glu Cys Ser His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly
                          - 2 -

Asp Glu Ile Val Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe
                405   410   415

Ser Thr Ser Glu Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu
                420   425   430

Leu Leu Glu Trp Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr
                435   440   445

Asn Asp Arg Arg Trp Glu Ser Ala Asp Leu Gln Glu Val Met Phe Thr
                450   455   460

Ala Leu Ile Lys Asp Arg Pro Lys Phe Val Arg Leu Phe Leu Glu Asn
465   470   475   480

Gly Leu Asn Leu Arg Lys Phe Leu Thr His Asp Val Leu Thr Glu Leu
                485   490   495

Phe Ser Asn His Phe Ser Thr Leu Val Tyr Arg Asn Leu Gln Ile Ala
                500   505   510

Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr Phe Val Trp Lys Leu Val
                515   520   525

Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu Asp Arg Asn Gly Arg Asp
                530   535   540

Glu Met Asp Ile Glu Leu His Asp Val Ser Pro Ile Thr Arg His Pro
545   550   555   560

Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu Gln Asn Lys Lys Glu Leu
                565   570   575

Ser Lys Val Ile Trp Glu Gln Thr Arg Gly Cys Thr Leu Ala Ala Leu
                580   585   590

Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala Lys Val Lys Asn Asp Ile
                595   600   605

Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala Asn Glu Tyr Glu Thr Arg
                610   615   620

Ala Val Glu Leu Phe Thr Glu Cys Tyr Ser Ser Asp Glu Asp Leu Ala

- 3 -

Glu Gln Leu Leu Val Tyr Ser Cys Glu Ala Trp Gly Gly Ser Asn Cys
              645   650   655

Leu Glu Leu Ala Val Glu Ala Thr Asp Gln His Phe Ile Ala Gln Pro
          660   665   670

Gly Val Gln Asn Phe Leu Ser Lys Gln Trp Tyr Gly Glu Ile Ser Arg
          675   680   685

Asp Thr Lys Asn Trp Lys Ile Ile Leu Cys Leu Phe Ile Ile Pro Leu
          690   695   700

Val Gly Cys Gly Phe Val Ser Phe Arg Lys Lys Pro Val Asp Lys His
705   710   715   720

Lys Lys Leu Leu Trp Tyr Tyr Val Ala Phe Phe Thr Ser Pro Phe Val
              725   730   735

Val Phe Ser Trp Asn Val Val Phe Tyr Ile Ala Phe Leu Leu Leu Phe
              740   745   750

Ala Tyr Val Leu Leu Met Asp Phe His Ser Val Pro His Pro Pro Glu
          755   760   765

Leu Val Leu Tyr Ser Leu Val Phe Val Leu Phe Cys Asp Glu Val Arg
          770   775   780

Gln Trp Tyr Val Asn Gly Val Asn Tyr Phe Thr Asp Leu Trp Asn Val
785   790   795   800

Met Asp Thr Leu Gly Leu Phe Tyr Phe Ile Ala Gly Ile Val Phe Arg
              805   810   815

Leu His Ser Ser Asn Lys Ser Ser Leu Tyr Ser Gly Arg Val Ile Phe
          820   825   830

Cys Leu Asp Tyr Ile Ile Phe Thr Leu Arg Leu Ile His Ile Phe Thr
          835   840   845

Val Ser Arg Asn Leu Gly Pro Lys Ile Ile Met Leu Gln Arg Met Leu
          850   855   860

Ile Asp Val Phe Phe Phe Leu Phe Leu Phe Ala Val Trp Met Val Ala

Phe Gly Val Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp
          885   890   895

Arg Trp Ile Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe
          900   905   910

Gly Gln Val Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His
          915   920   925

Cys Thr Phe Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp
     930   935   940

Glu His Asn Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val
945   950   955   960

Cys Ile Tyr Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val
               965   970   975

Ala Met Phe Gly Tyr Thr Val Gly Thr Val Gln Glu Asn Asn Asp Gln
               980   985   990

Val Trp Lys Phe Gln Arg Tyr Phe Leu Val Gln Glu Tyr Cys Ser Arg
     995   1000   1005

Leu Asn Ile Pro Phe Pro Phe Ile Val Phe Ala Tyr Phe Tyr Met
     1010   1015   1020

Val Val Lys Lys Cys Phe Lys Cys Cys Cys Lys Glu Lys Asn Met
     1025   1030   1035

Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp Asn Glu Thr Leu
     1040   1045   1050

Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val Lys Ile Asn
     1055   1060   1065

Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg Phe Arg
     1070   1075   1080

Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys Glu
     1085   1090   1095

Ile Ala Asn Lys Ile Lys

```
<210>    2
<211>    3315
<212>    DNA
<213>    Homo sapiens

<400>    2
atgtcctttc gggcagccag gctcagcatg aggaacagaa ggaatgacac tctggacagc      60

acccggaccc tgtactccag cgcgtctcgg agcacagact tgtcttacag tgaaagcgac     120

ttggtgaatt ttattcaagc aaattttaag aaacgagaat gtgtcttctt taccaaagat     180

tccaaggcca cggagaatgt gtgcaagtgt ggctatgccc agagccagca catggaaggc     240

acccagatca accaaagtga gaaatggaac tacaagaaac acaccaagga atttcctacc     300

gacgcctttg gggatattca gtttgagaca ctggggaaga aagggaagta tatacgtctg     360

tcctgcgaca cggacgcgga atcctttac gagctgctga cccagcactg gcacctgaaa     420

acacccaacc tggtcatttc tgtgaccggg ggcgccaaga acttcgccct gaagccgcgc     480

atgcgcaaga tcttcagccg gctcatctac atcgcgcagt ccaaaggtgc ttggattctc     540

acgggaggca cccattatgg cctgatgaag tacatcgggg aggtggtgag agataacacc     600

atcagcagga gttcagagga gaatattgtg gccattggca tagcagcttg gggcatggtc     660

tccaaccggg acaccctcat caggaattgc gatgctgagg ctattttt agcccagtac     720

cttatggatg acttcacaag agatccactg tatatcctgg acaacaacca cacacatttg     780

ctgctcgtgg acaatggctg tcatggacat cccactgtcg aagcaaagct ccggaatcag     840

ctagagaagt atatctctga gcgcactatt caagattcca actatggtgg caagatcccc     900

attgtgtgtt ttgcccaagg aggtggaaaa gagactttga aagccatcaa tacctccatc     960

aaaaataaaa ttccttgtgt ggtggtggaa ggctcgggcc agatcgctga tgtgatcgct    1020

agcctggtgg aggtggagga tgccctgaca tcttctgccg tcaaggagaa gctggtgcgc    1080

ttttacccc gcacggtgtc ccggctgcct gaggaggaga ctgagagttg gatcaaatgg    1140

ctcaaagaaa ttctcgaatg ttctcaccta ttaacagtta ttaaaatgga agaagctggg    1200

gatgaaattg tgagcaatgc catctcctac gctctataca aagccttcag caccagtgag    1260

caagacaagg ataactggaa tgggcagctg aagcttctgc tggagtggaa ccagctggac    1320

ttagccaatg atgagatttt caccaatgac cgccgatggg agtctgctga ccttcaagaa    1380

gtcatgttta cggctctcat aaaggacaga cccaagtttg tccgcctctt tctggagaat    1440

ggcttgaacc tacggaagtt tctcacccat gatgtcctca ctgaactctt ctccaaccac    1500

ttcagcacgc ttgtgtaccg gaatctgcag atcgccaaga attcctataa tgatgccctc    1560
```

```
ctcacgtttg tctggaaact ggttgcgaac ttccgaagag gcttccggaa ggaagacaga    1620

aatggccggg acgagatgga catagaactc cacgacgtgt ctcctattac tcggcacccc    1680

ctgcaagctc tcttcatctg ggccattctt cagaataaga aggaactctc caaagtcatt    1740

tgggagcaga ccaggggctg cactctggca gccctgggag ccagcaagct tctgaagact    1800

ctggccaaag tgaagaacga catcaatgct gctggggagt ccgaggagct ggctaatgag    1860

tacgagaccc gggctgttga gctgttcact gagtgttaca gcagcgatga agacttggca    1920

gaacagctgc tggtctattc ctgtgaagct tggggtggaa gcaactgtct ggagctggcg    1980

gtggaggcca cagaccagca tttcatcgcc cagcctgggg tccagaattt tcttcctaag    2040

caatggtatg gagagatttc ccgagacacc aagaactgga agattatcct gtgtctgttt    2100

attataccct tggtgggctg tggctttgta tcatttagga agaaacctgt cgacaagcac    2160

aagaagctgc tttggtacta tgtggcgttc ttcacctccc ccttcgtggt cttctcctgg    2220

aatgtggtct tctacatcgc cttcctcctg ctgtttgcct acgtgctgct catggatttc    2280

cattcggtgc cacacccccc cgagctggtc ctgtactcgc tggtctttgt cctcttctgt    2340

gatgaagtga cacagtggta cgtaaatggg gtgaattatt ttactgacct gtggaatgtg    2400

atggacacgc tggggctttt ttacttcata gcaggaattg tatttcggct ccactcttct    2460

aataaaagct ctttgtattc tggacgagtc attttctgtc tggactacat tattttcact    2520

ctaagattga tccacatttt tactgtaagc agaaacttag gacccaagat tataatgctg    2580

cagaggatgc tgatcgatgt gttcttcttc ctgttcctct ttgcggtgtg gatggtggcc    2640

tttggcgtgg ccaggcaagg gatccttagg cagaatgagc agcgctggag gtggatattc    2700

cgttcggtca tctacgagcc ctacctggcc atgttcggcc aggtgcccag tgacgtggat    2760

ggtaccacgt atgactttgc ccactgcacc ttcactggga atgagtccaa gccactgtgt    2820

gtggagctgg atgagcacaa cctgccccgg ttccccgagt ggatcaccat ccccctggtg    2880

tgcatctaca tgttatccac caacatcctg ctggtcaacc tgctggtcgc catgtttggc    2940

tacacggtgg gcaccgtcca ggagaacaat gaccaggtct ggaagttcca gaggtacttc    3000

ctggtgcagg agtactgcag ccgcctcaat atccccttcc ccttcatcgt cttcgcttac    3060

ttctacatgg tggtgaagaa gtgcttcaag tgttgctgca aggagaaaaa catggagtct    3120

tctgtctgct gtttcaaaaa tgaagacaat gagactctgg catgggaggg tgtcatgaag    3180

gaaaactacc ttgtcaagat caacacaaaa gccaacgaca cctcagagga aatgaggcat    3240

cgatttagac aactggatac aaagcttaat gatctcaagg gtcttctgaa agagattgct    3300

aataaaatca aatga                                                      3315
```
- 7 -